

1/10

```

hFRS2: 1 MGSCCSCPKDTPVDNHRNKFVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYL
mFRS2: M-----V-----
hFRS3: 1 MGSCCSCLNRDSPVDNHPTKFKVTNVDDGVELGSGVMELTQSELVLHLHRREAVRWPYL
mFRS3: M--W--D-----H-----Q-----
      **** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

hFRS2: 61 CLRRYGYDSNLFSESGRRRCQTGGIFAFKCARAEELFNMLQEIMQNNNSINVVEEPVVE
mFRS2: -----
hFRS3: 61 CLRRYGYDSNLFSESGRRRCQTGGIFAFKCSRAEEIFNLLQDLMQCNSINVMEEPVIIT
mFRS3: -----D-----T-----
      ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

hFRS2: 120 RNNHQTELEVPRTPTPTTPGFAAQNLPNGYPRYPSFGDASSHPSSRHPSPVGSARLPSVG
mFRS2: -SS-----LG-----
hFRS3: 121 RNSHPAELDLPRAP QPPNALGYTVSSFSNGCP GEGPRFSAPRRLSTSSLRHPSLG
mFRS3: -S--P-----G-P--AGYTVSGF-NGFP--P-----P-----
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Grb2
hFRS2: 180 EESTHPLLVAEEQVHTYVNTTGVQEERKNRTSVHVPLEARVSNAESSTPKKEPSSIEDRD
mFRS2: -----A-----P-----N-----NP-----
hFRS3: 176 EESTHALIAPDEQSHTYVNTPASEDDHRRGRHCLQPLPE GOAPFLPOARGP DQRD
mFRS3: -----T--SE-----TGDE-G-S-----RV-LPA-TQ-S-----
      ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

hFRS2: 240 PQILLEPEGVKFVLGPTPVQKQIMEKEKLEQLGRDQVSGSGANNTTEWDTGYDSDERRDAP
mFRS2: --V--K--R-----K-P-----G-----V-----
hFRS3: 231 PQVFLQPGQVKFVLGPTPARRHMVKCGLCPSLHDPHHNNNEAP SECP
mFRS3: ---L-----QVM--S--GMQ-----G-----
      ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Grb2 Grb2
hFRS2: 300 SVNKLVEENINGLSIPSASGVRRGRLTSTSTSDTQININNSAQRRTALLNYENLPSLPVW
mFRS2: P-----P-----
hFRS3: 281 AQPCKTYENVTG GLWRGAGWRLSPEEPGWNGLAHRRRAALLHYENLPPLPPVW
mFRS3: -----S-- --QQ-----R--S-----
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Grb2
hFRS2: 360 EARKLSRDEDDNLGPKTPSLNGYHNNLDPMHNYVNTENVTPASAHKIEYSR
mFRS2: -----D--K
hFRS3: 333 ESQAQQLGGEAGDDGDSRDGLTPSSNGFPDGEEDETPLQKPTSTRAAIRSHGSFPVPLTR
mFRS3: --G--P-----SA--SG-----
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SH-PTP2
hFRS2: 412 RRDCTPTVFNFDIRRPSLEH RQLNYIQVDLEGGSDSDNPQTPKTPPTPLPQTPTRR
mFRS2: -----
hFRS3: 393 RRG SPRVFNFDFRRPGPEPPRQLNYIQVELKGWGGDRPKGPQNPPSQAPMPTTHPARS
mFRS3: ---Q-----TA-----VSG--G--P--V--
      ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SH-PTP2
hFRS2: 468 TELYAVIDIERTAAMSNLQKALPRDDGTSRKTRHNSTDLP 508
mFRS2: -----
hFRS3: 452 SDSYAVIDLKKTVAMSNLQALPRDDGTARKTRHNSTDLP 492
mFRS3: -----A--D-----AV-----
      ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

FIGURE 1

2/10

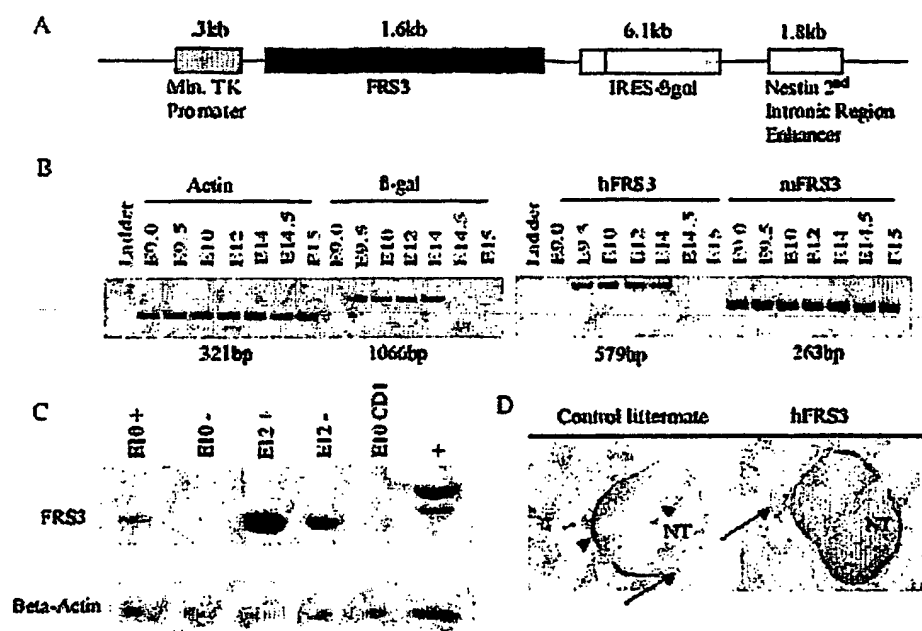


FIGURE 2

3/10

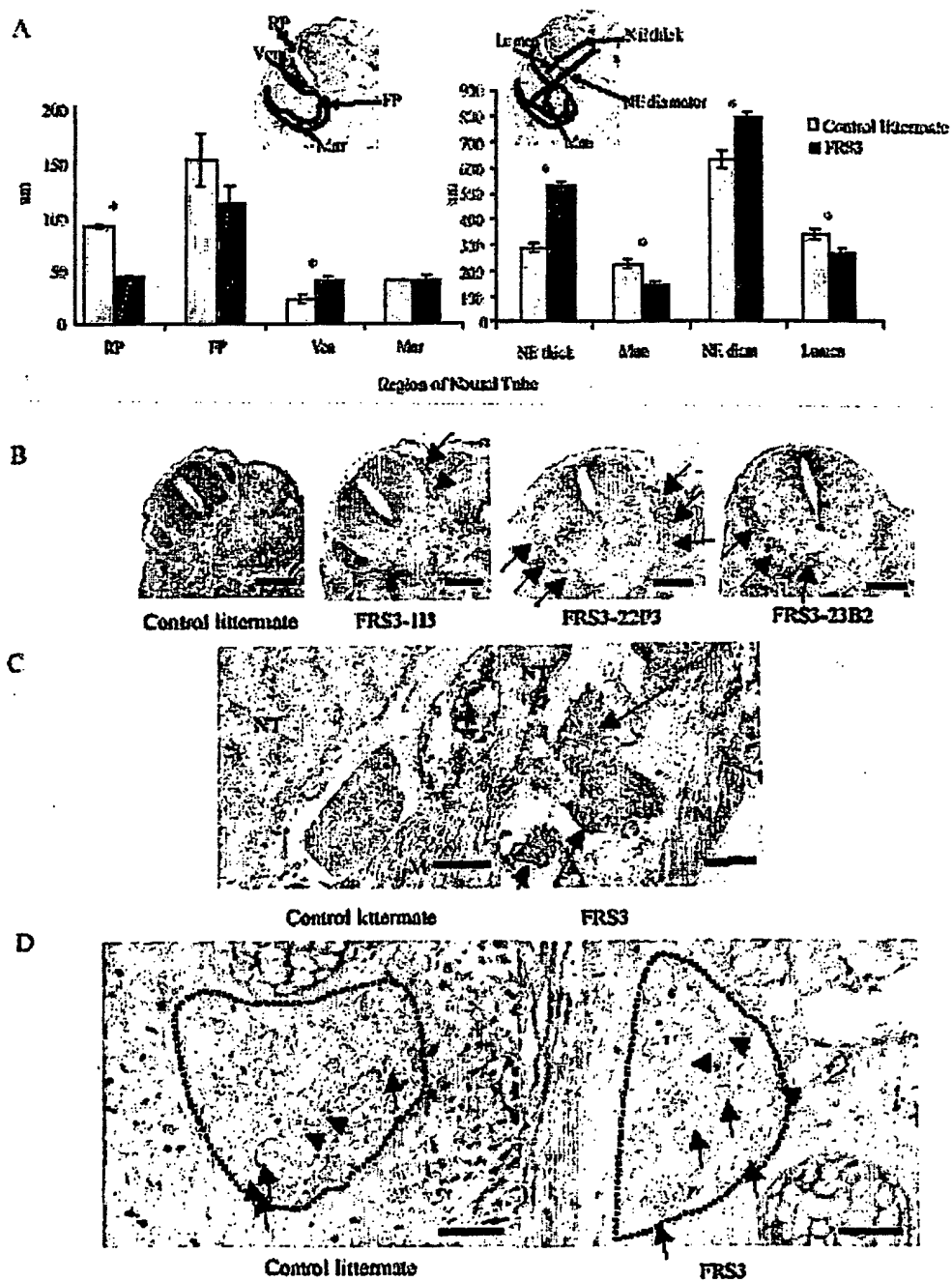
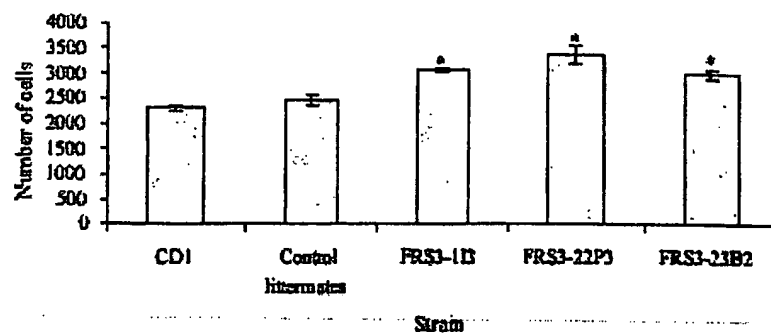
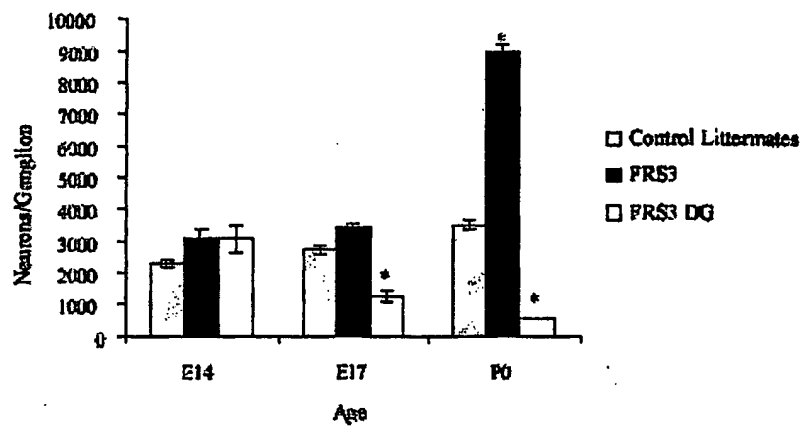


FIGURE 3

4/10

**A****B****FIGURE 4**

5/10

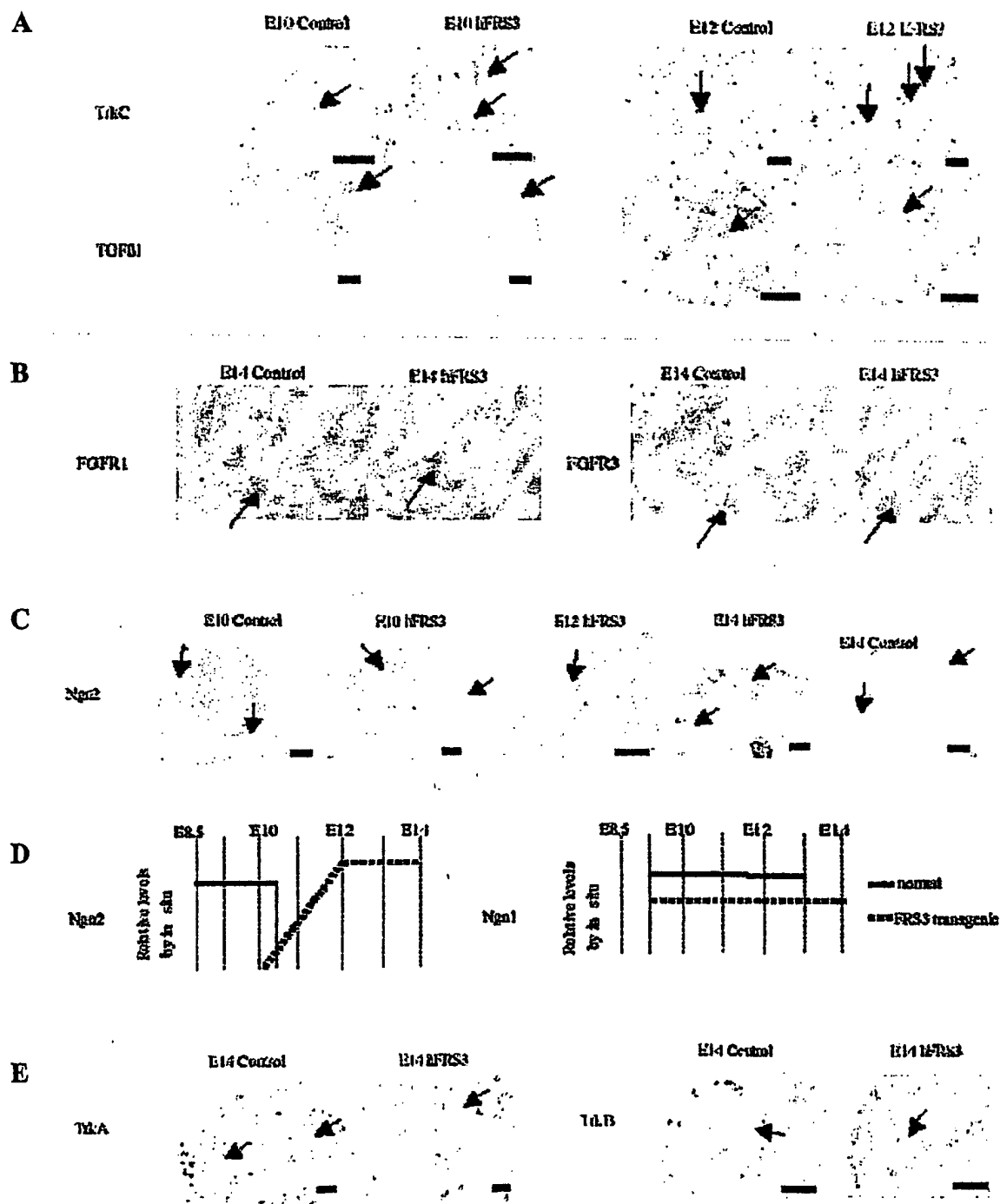


FIGURE 5

6/10

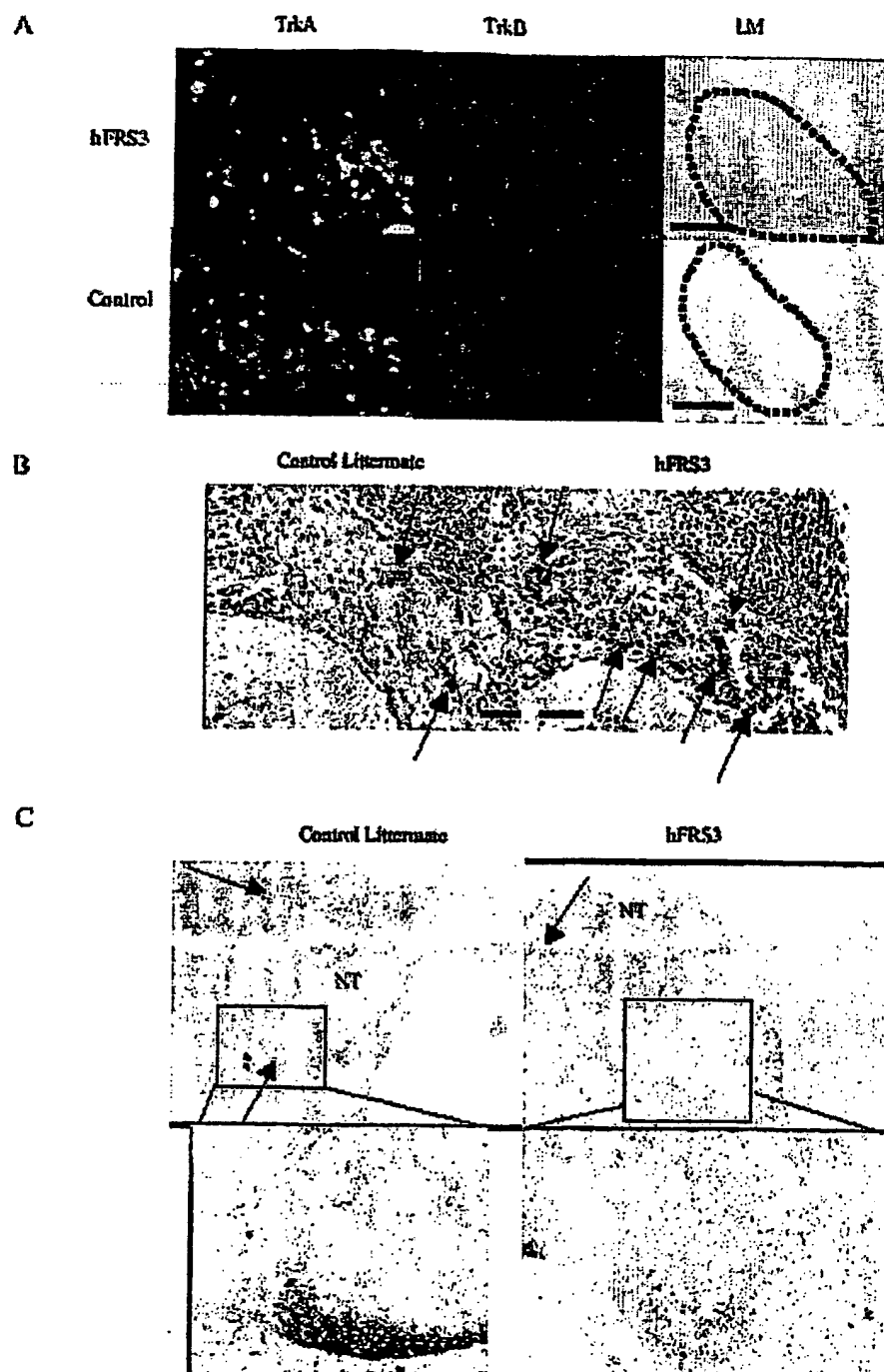


FIGURE 6

7/10

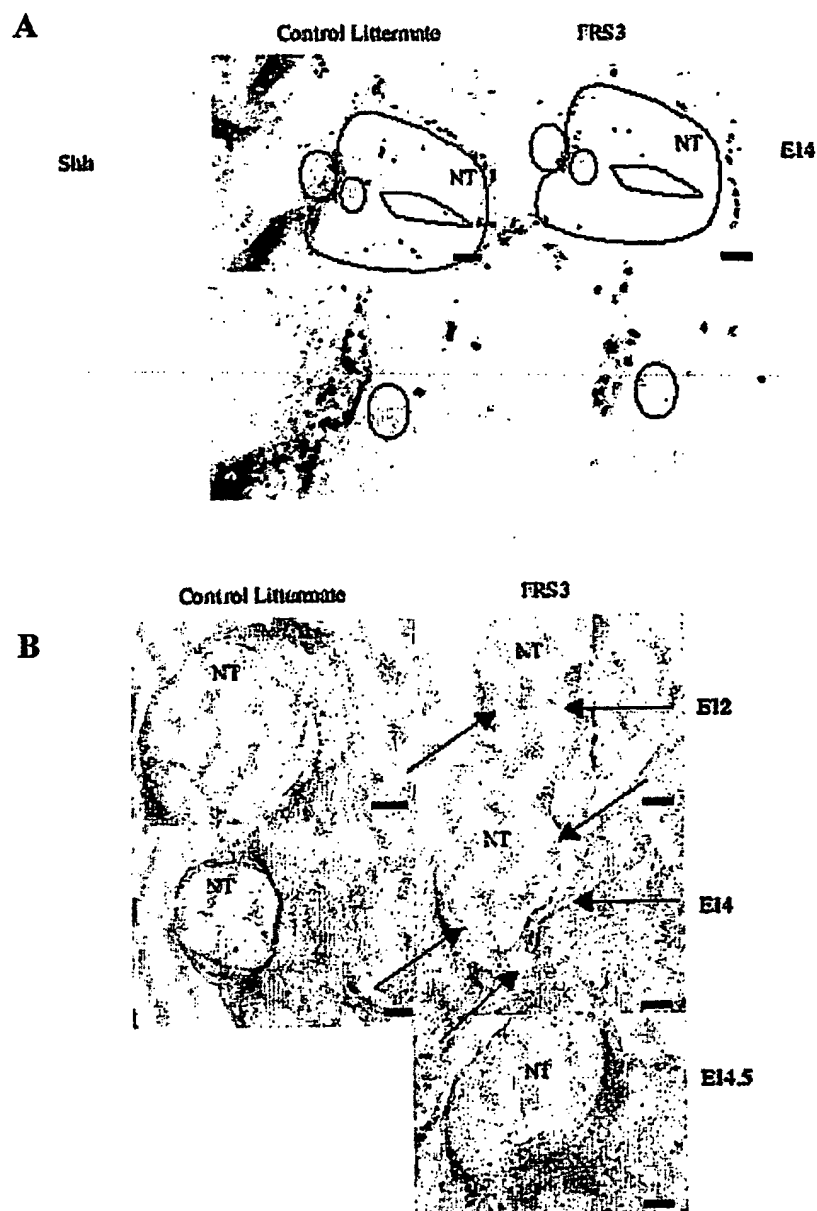
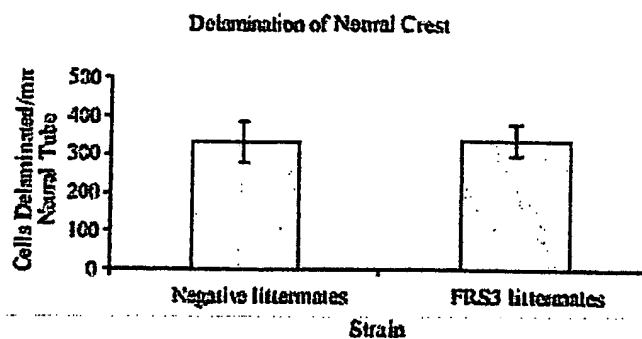


FIGURE 7

8/10

A



B

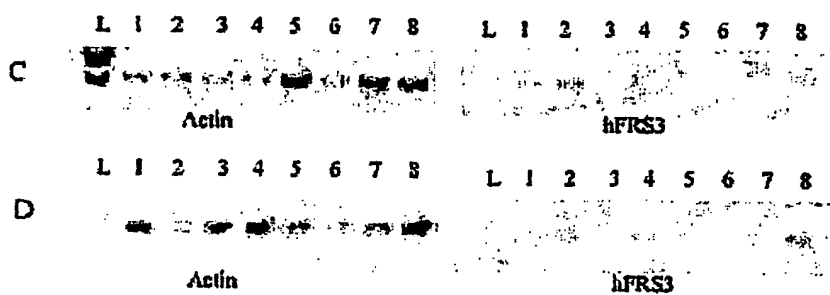
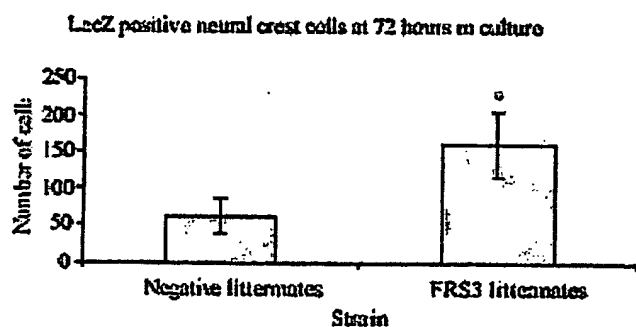


FIGURE 8



9/10

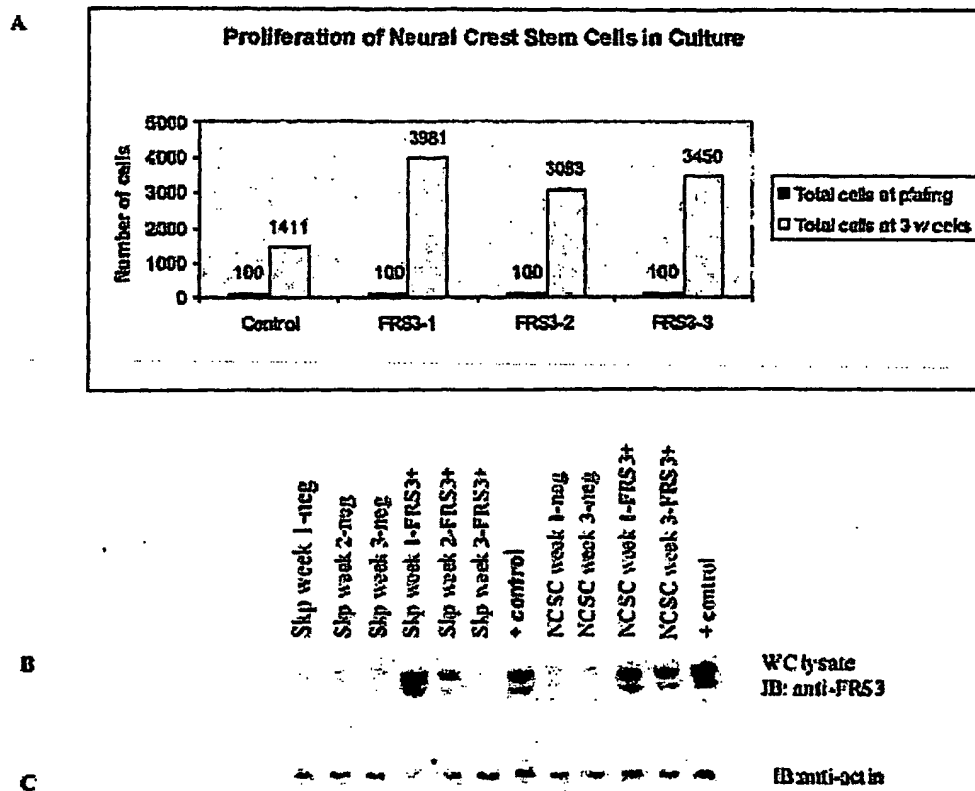


FIGURE 9

10/10

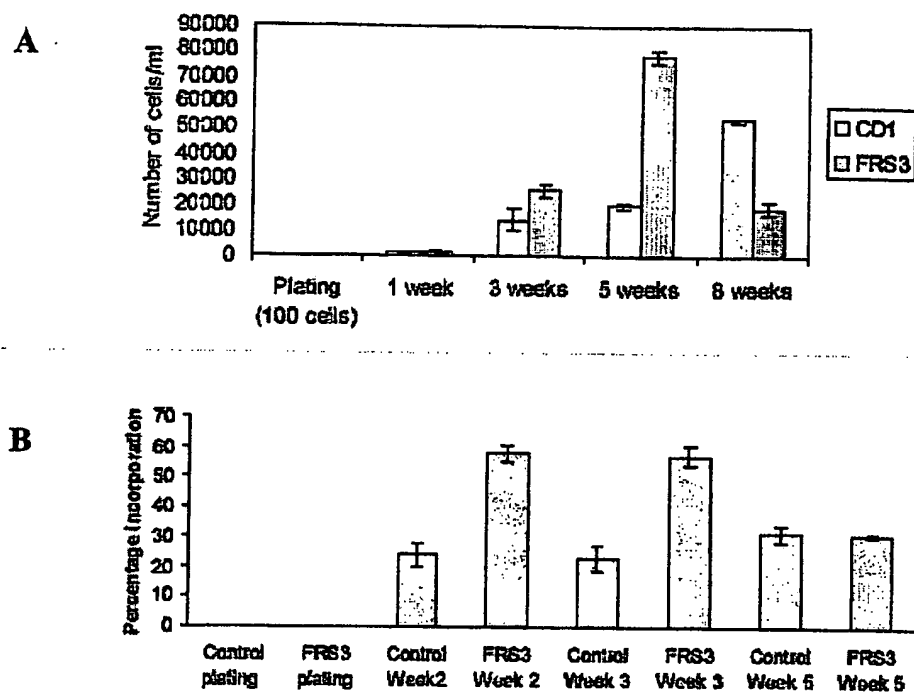


FIGURE 10

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